

## 多抗菌剂对植烟土壤细菌群落多样性的影响

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**摘要:** 454 :  
(Proteobacteria) (Actinobacteria) (Acidobacteria)  
(Gemmatimonadetes) (Firmicutes)  
7.27% OTU 12.83% 4.62% OTU  
20.31%

**关键词:** ; ; 454 ;  
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## The Effect of Multiple Antimicrobial Inoculant on the Bacterial Community Diversity in Tobacco Planting Soil

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**Abstract:** We used 454 pyrophosphate sequencing approach to analyze the bacterial community structure of the tobacco planting soils with multiple antimicrobial inoculant. The results showed that the bacterium in tobacco planting soil which was detected in this experiment belong to five phyla. They are Proteobacteria, Actinobacteria, Acidobacteria, Gemmatimonadetes, Firmicutes compared with rizosphere soil without using multiple antimicrobial inoculants, the number of class which belonged to rizosphere soil with multiple antimicrobial inoculant reduced 7.27%, and the number of OTU reduced 12.83%. Compared with non-rizosphere soil without using multiple antimicrobial inoculants, the number of class which belonged to non-rizosphere soil with multiple antimicrobial inoculant reduced 4.62%, and the number of OTU reduced 20.31%. Obviously, multiple antimicrobial inoculants can lead the decrease in microbial diversity of tobacco planting soil.

**Keywords:** Tobacco planting soil; bacterial community diversity; 454 pyrophosphate sequencing; multiple antimicrobial inoculant

*Ralstonia solanacearum*

[1]

[2]

[3-5]

[6]

[7]

[8]

DGGE(

)<sup>[9]</sup>

PCR

DNA

DNA

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T-RFLP [10,11] FAME  
 PLFA  
 454 Illumina 454  
 454 [12,13] 100 400~500 bp  
*Brevibacillus brevis* DZQ3  
*Paenibacillus polymyxa* YD0136  
*Paenibacillus polymyxa* YD0573  
 454

1 材料与方法

1.1 取样

1264 m 2013 7 28 107.6° 28.89°  
 S1 S2 S3 S4  
 -20

1.2 样品处理

DNA DNA OMEGA E.Z.N.A. Soil DNA Kit  
 DNA  
 454 GX-FLX Roche

2 结果分析

1

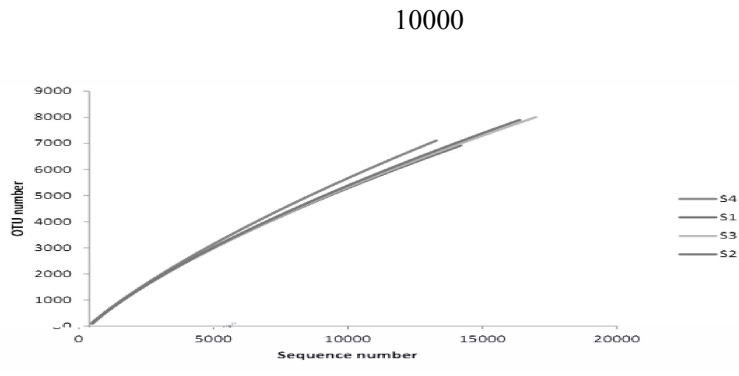


图1 稀释曲线  
 Fig.1 Dilution curve

2.1 丰度及多样性评估

ACE Chao OTU 1  
 S2 ACE Chao S1 ACE Chao S4 ACE  
 S3 ACE S4 Chao S3 Chao S2 S3 S4 S1 Shanon  
 OTU S3 S2 S4 S1

表1 样本的多样性指数 (97%相似水平)

Table 1 The community index (97%similarity level)

Treatments	(Shanon)	(Chao)	(ACE)
	Community diversity index	Community abundance index	Community abundance index
S1	8.214612	20399.06	39544.61
S2	8.280843	24178.55	47926.8
S3	8.27974	23932.74	44203.52
S4	8.266288	23265.82	46404.18

Shannon S2 S3 S4 S1 Shanon α- Shannon S3

2.2 分类统计

OTU S1 S2 S3 S4 30  
 29 23 26 62 65 55 51 98 98 87 78  
 155 152 139 131 225 235 234 210  
 S1 S2 4.62% S4 S3 7.27%

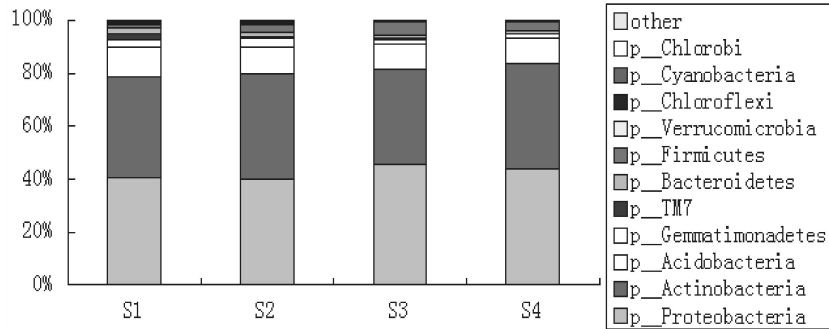


图 2 样本的群落结构相对丰度 (门水平)

Fig.2 The relative abundance of bacterial in phylum level

2 Proteobacteria Actinobacteria  
 Acidobacteria Gemmatimonadetes Firmicutes  
 S1 S2 S3 S4 93.9% 96.4% 97.4% 98.0% Gemmatimonadetes  
 Firmicutes Gemmatimonadetes  
 S1 2.9% S2 3.5% S3 1.85% S4 1.49%  
 Firmicutes S3 4.6% S4 3.3% S1 1.3% S2 3.0%  
 S1 Spirochaetes) S2  
 Tenericutes S4 LCP-89 (S1&S2)  
 Deferribacteres GN04 Synergistetes (S3&S4)  
 Fibrobacteres  
 Proteobacteria α-  
 Alphaproteobacteria S1 S2 S3 S4 66.9% 69.1% 50.3% 63.9%  
 γ- Gammaproteobacteria 27.05%  
 10.68% S2 S3 S2 TA18  
 S3 ε- Epsilonproteobacteria

2.3 β多样性评估

3 S1 OTU 4249 S2 OTU 5332 S3  
 OTU 4997 S4 OTU 4356 S1 OTU  
 S2 OTU 20.31% S4 OTU  
 S3 OTU 12.83%  
 S1 OTU 1592 S2 OTU 2763 S3 OTU  
 1939 S4 OTU 1578 S1 S2 OTU 1694 S3 S4  
 OTU 2012 S1 S4 OTU 1454 S2 S3 OTU 1523

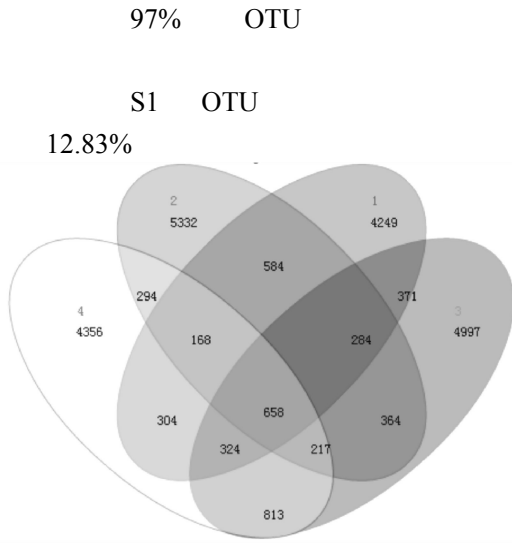


图3 样品共有和特有的 OTU 数目 (97%相似水平)  
Fig.3 The amount of common and peculiar OTU in four samples (97% similarity level)

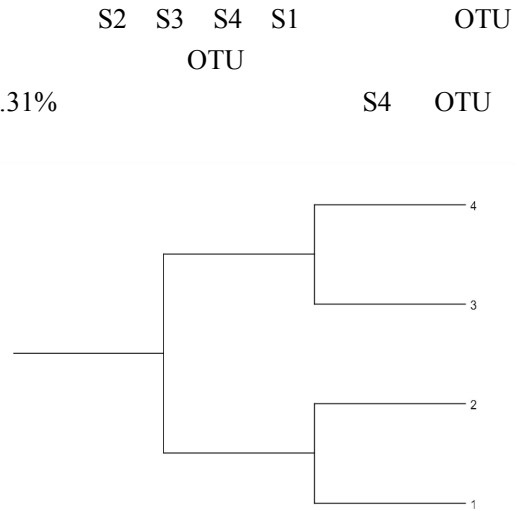


图4 样品的群落结构相似度树状图(97%相似水平)  
Fig.4 The tree of community structural similarity (97%similarity level)

注: 图中 1 表示样品 S1; 2 表示样品 S2; 3 表示样品 S3; 4 表示样品 S4  
Note: 1 represents the sample S1, 2 represents the sample S2, 3 represents the sample S3, and 4 represents the sample S4

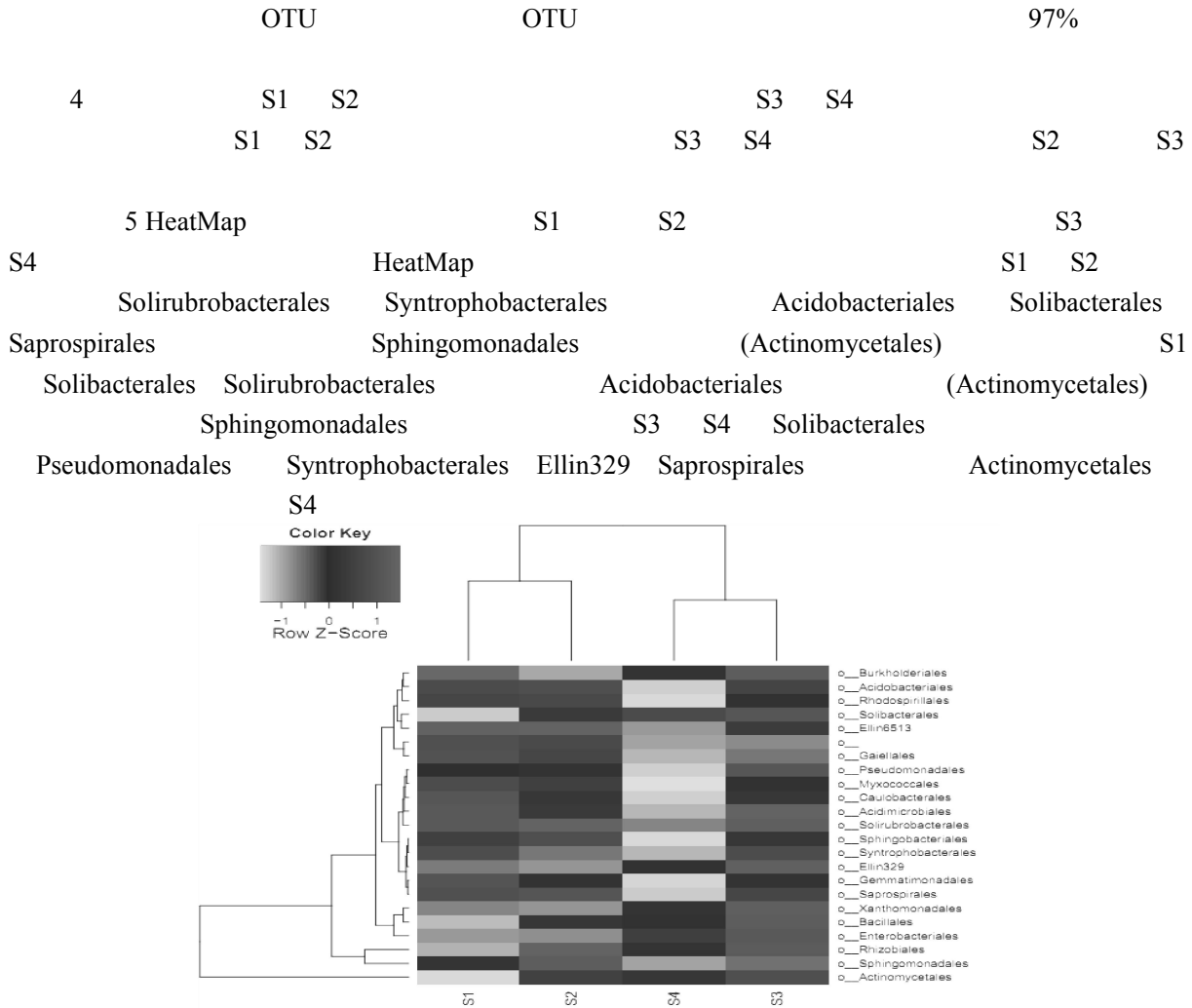


图5 样品的聚类分析图 (目水平)  
Fig.5 The clustering analysis of bacterial in order level

### 3 结论与讨论

[7]

7.3~13.4 [14]

S3 S4 ACE Chao

### 参考文献

[1] Hayward AC. Biology and epidemiology of bacterial wilt caused by *Ralstonia solanacearum*[J]. Annu Rev Phytopathol, 1991,29:65-87

[2] , , . [J]. ( ),2008,30(S1):31-35

[3] , . [J]. ,2009(4):91-93,94

[4] , . [J]. ,2001,16(1):72-76

[5] , , . [J]. ,2001(9):44-48

[6] , , . [J]. ,2014,20(5):1203-1211

[7] . [D]. : ,2012

[8] , , , . [J]. ,2011,17(1):166-174

[9] , , , . DGGE T-RFLP [J]. ,2007,5:31-33

[10] , , . T-RFLP [J]. ,2009,36(7):75-78

[11] , , . T-RFLP [J]. ,2004,28(3):64-68

[12] , , . CVTree 454 [J]. ,2010,22(4):312-316

[13] , . 454 [J]. ,2013(8):203-205

[14] , , . [J]. ,2008,45(6):1095-1101